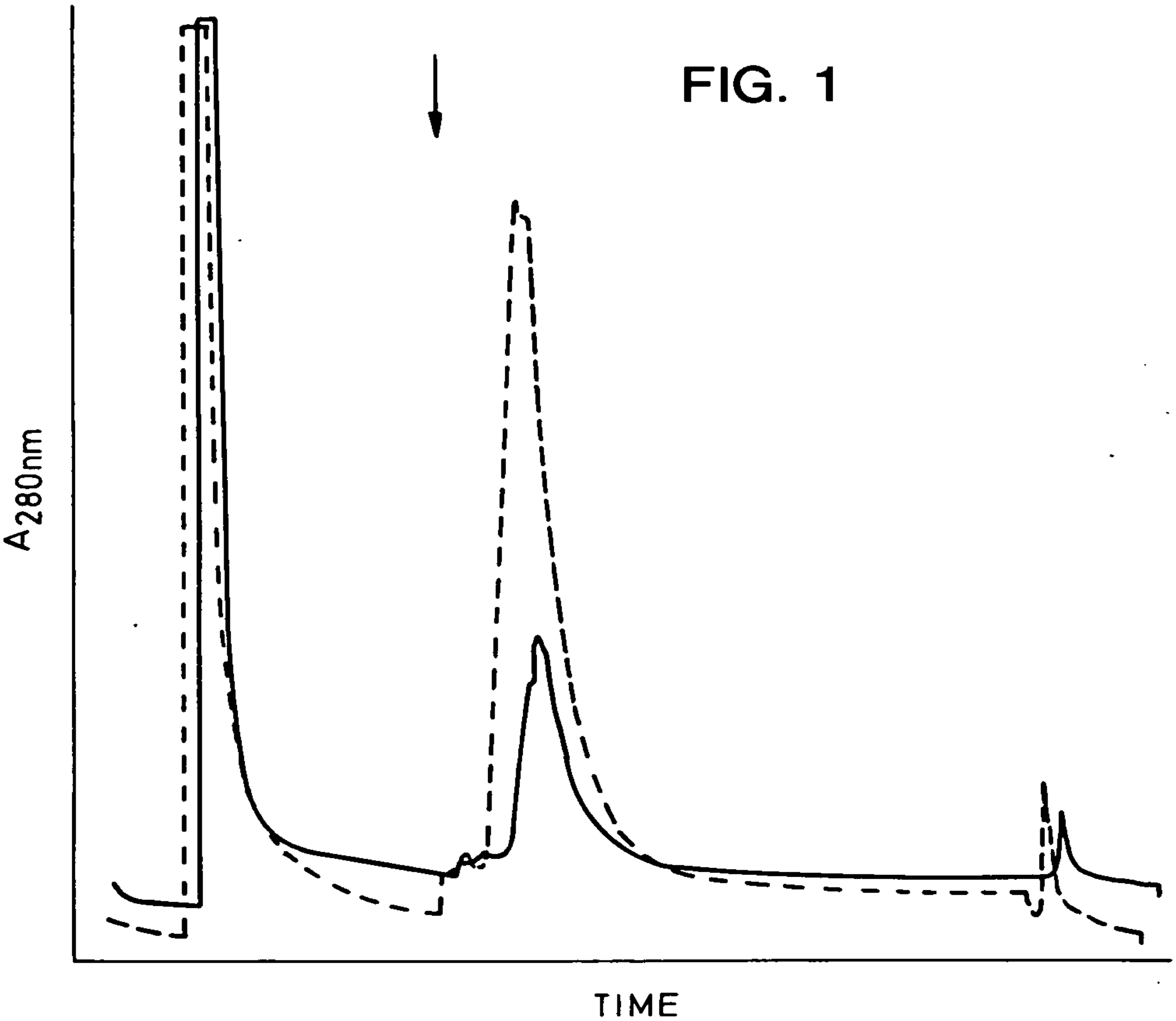


FIG. 1

FIG. 2A

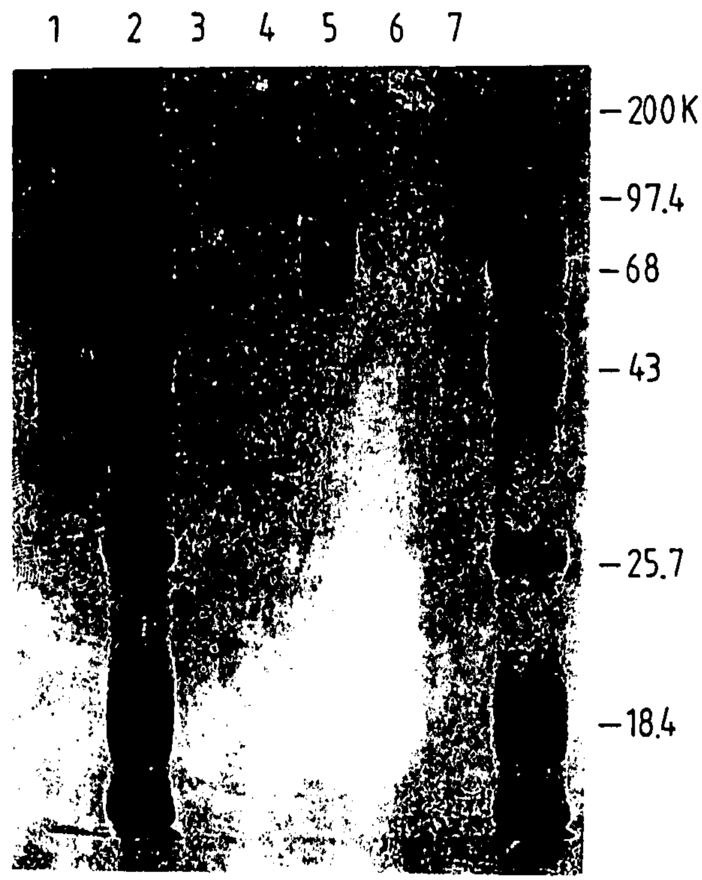


FIG. 2B

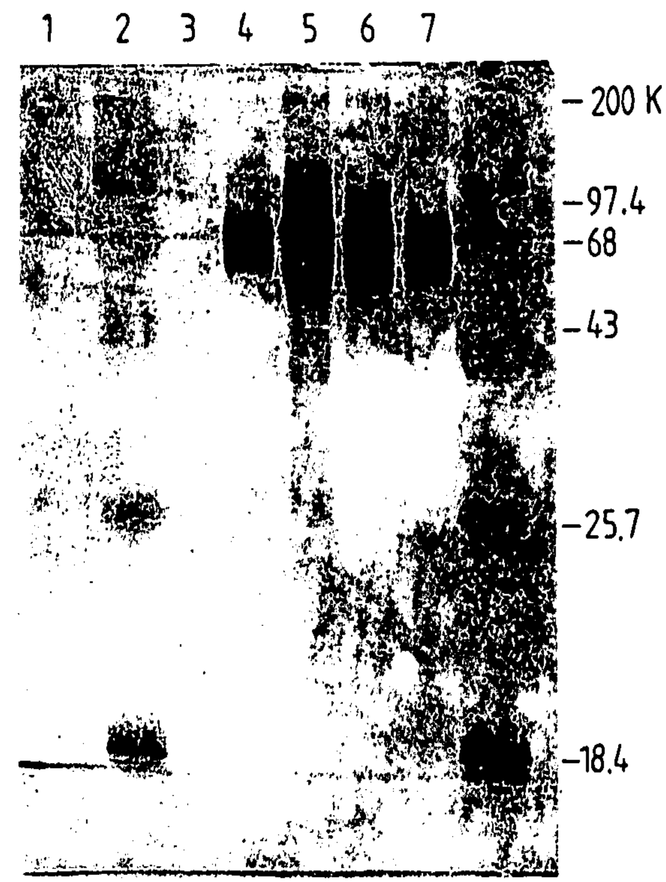


FIG. 3

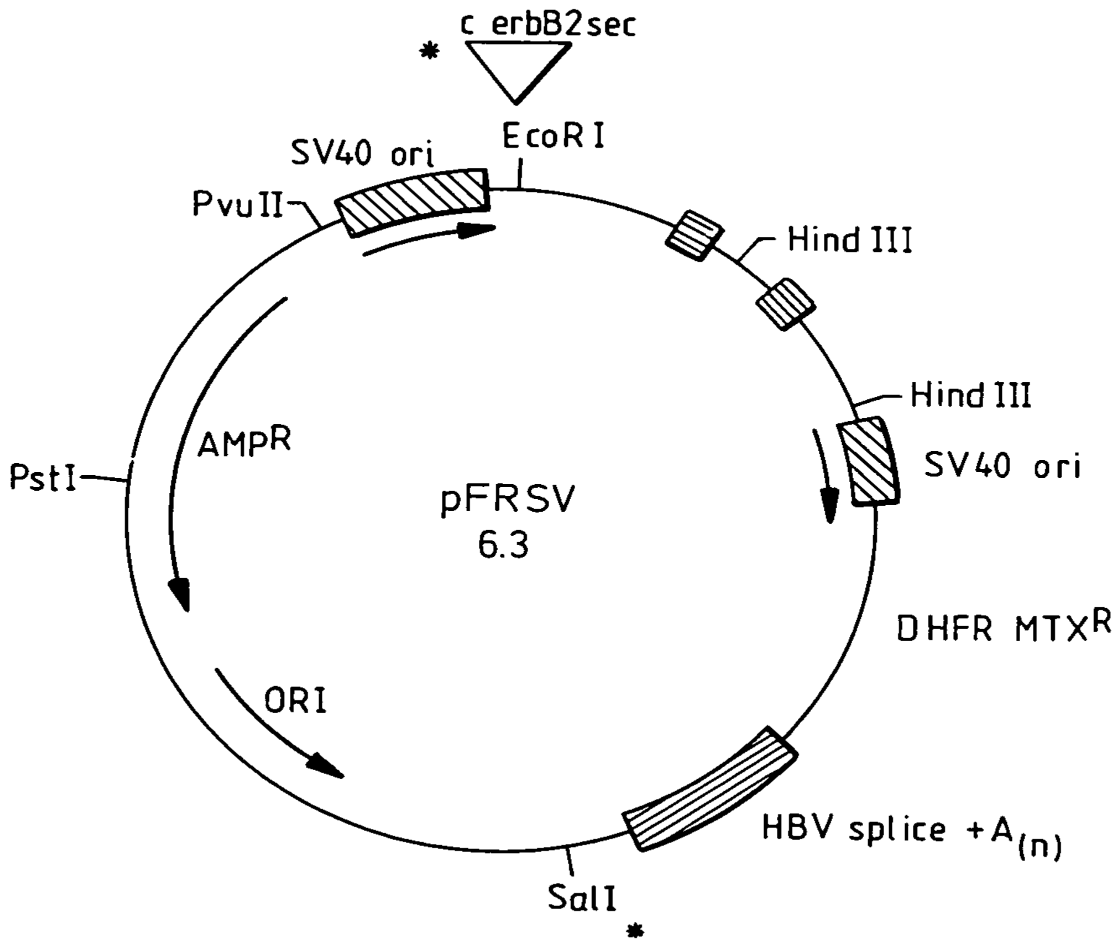
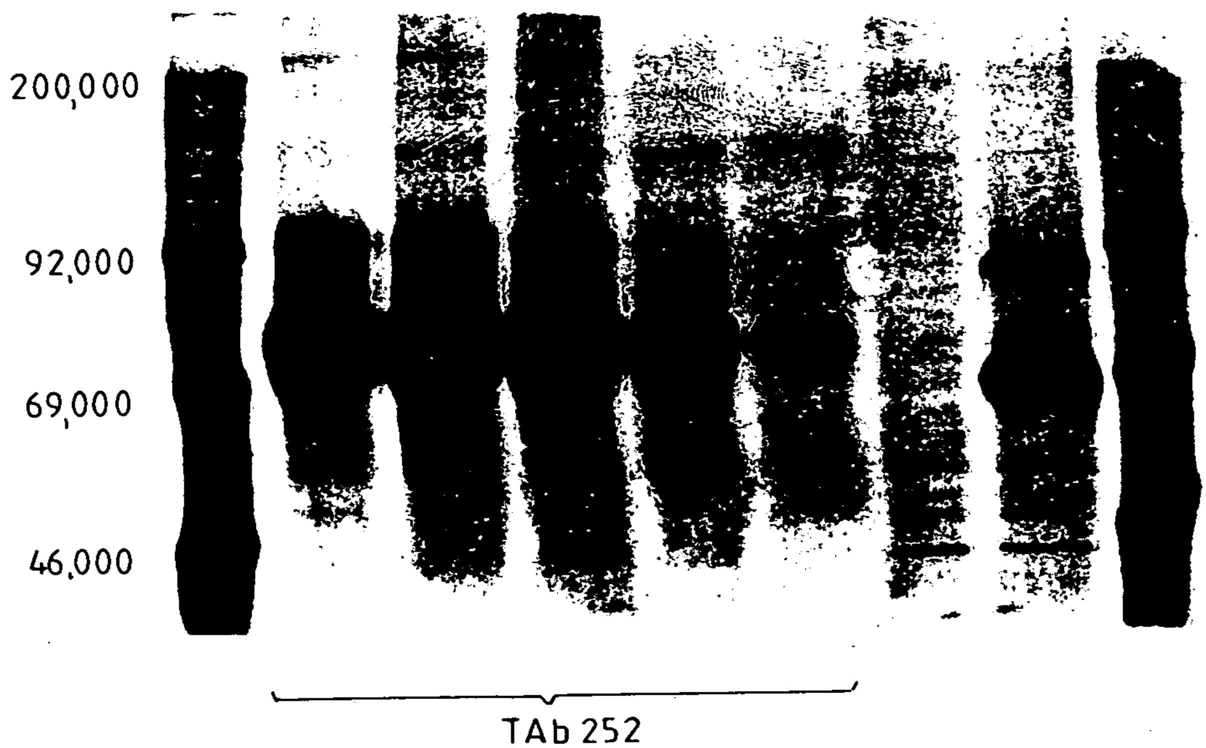

c erbB2sec
*
EcoR I
SV40 ori
PvuII
Hind III
Hind III
SV40 ori
PstI
AMPR
pFRSV
6.3
DHFR MTXR
ORI
HBV splice +A(n)
SalI
*

FIG. 4



NIH3T3-c-erbB-2 lysate + S35 labeled c1.4-3 supernatant

FIG. 5

Radioimmunoprecipitation of gp75 from SKBR3 Supernatant

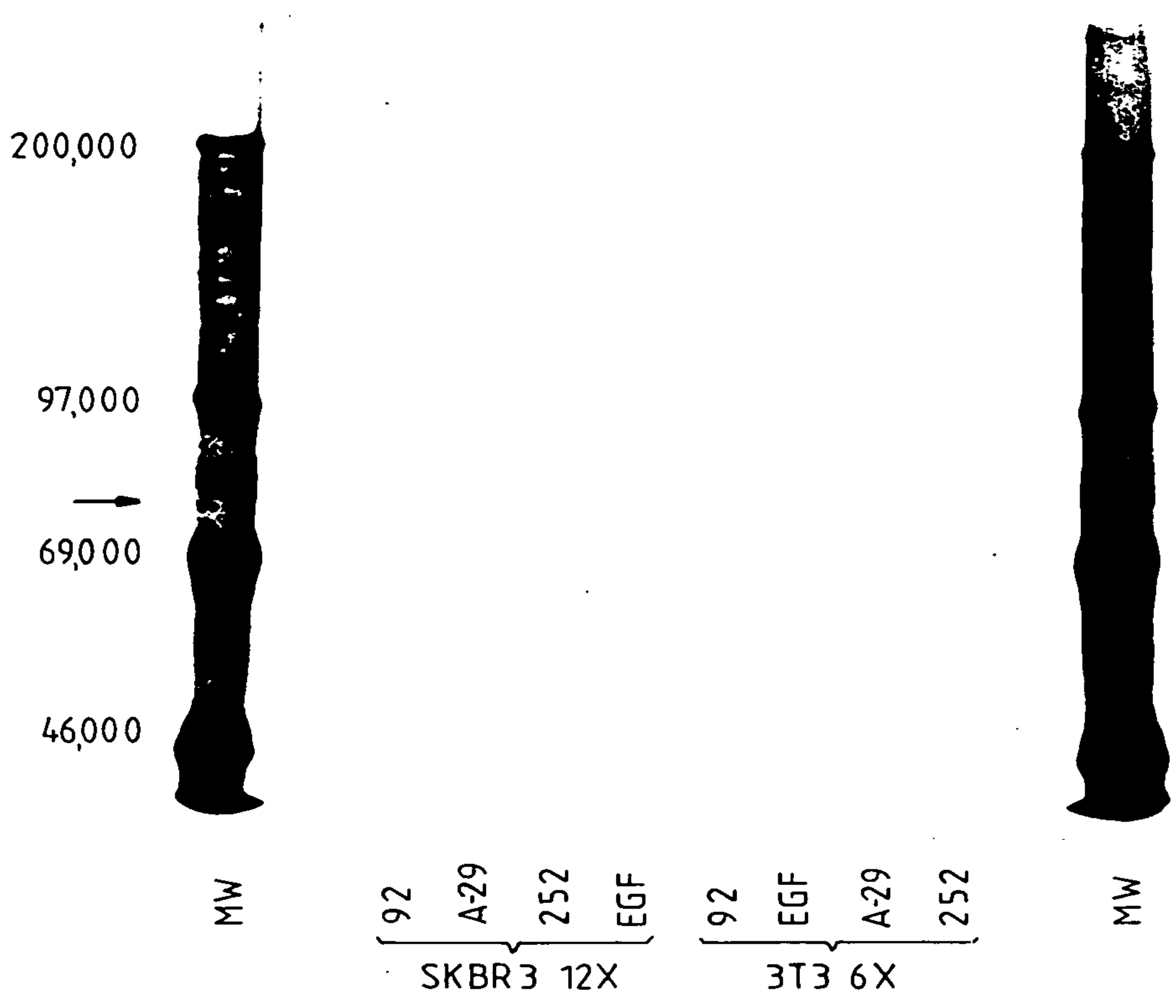


FIG. 6

Radioimmunoprecipitation of Supernatants From Various Cell Lines

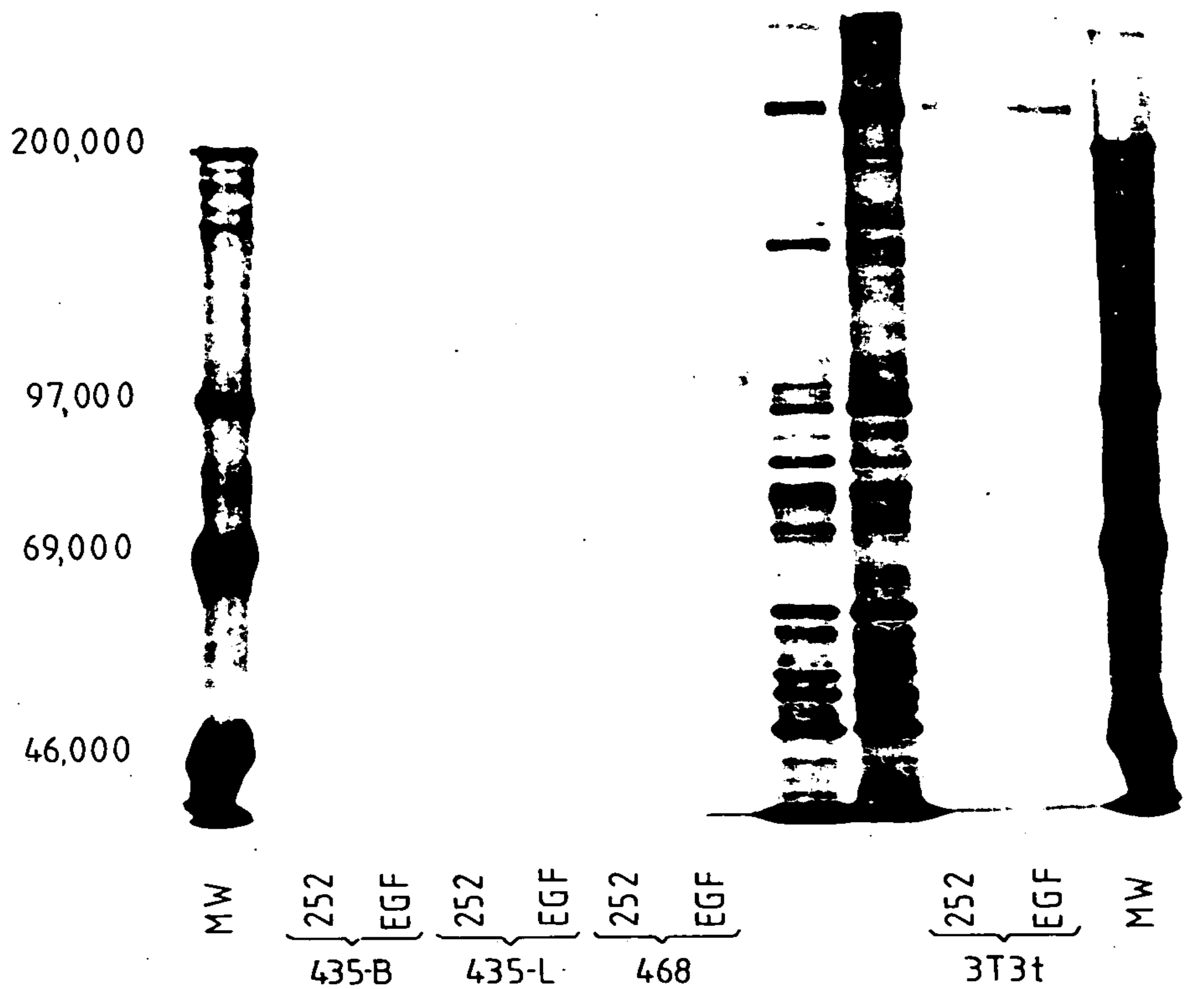


FIG. 7

Comparison of Standards in Sandwich IRMA

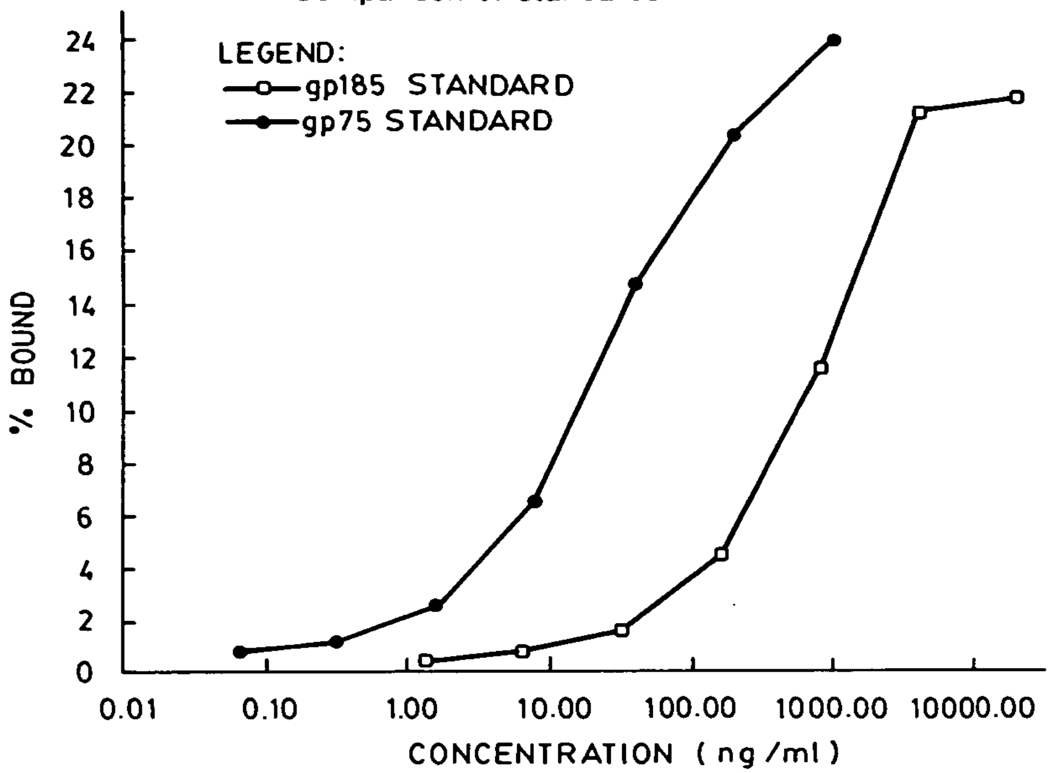


FIG. 8

Analysis of Nude Mouse Sera In c-erbB-2 IRMA

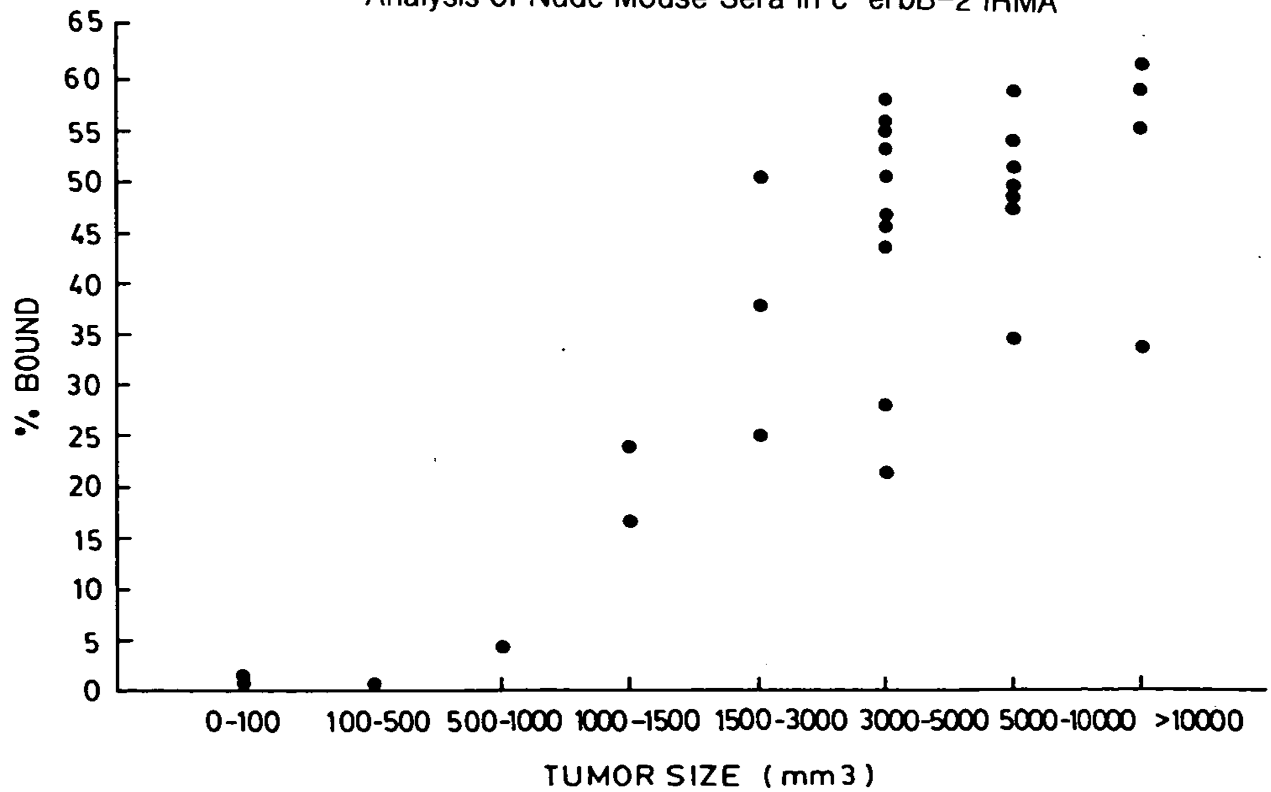


FIG. 9

Analysis of Nude Mouse Sera in the c–erbB–2 IRMA
Treated vs. Untreated

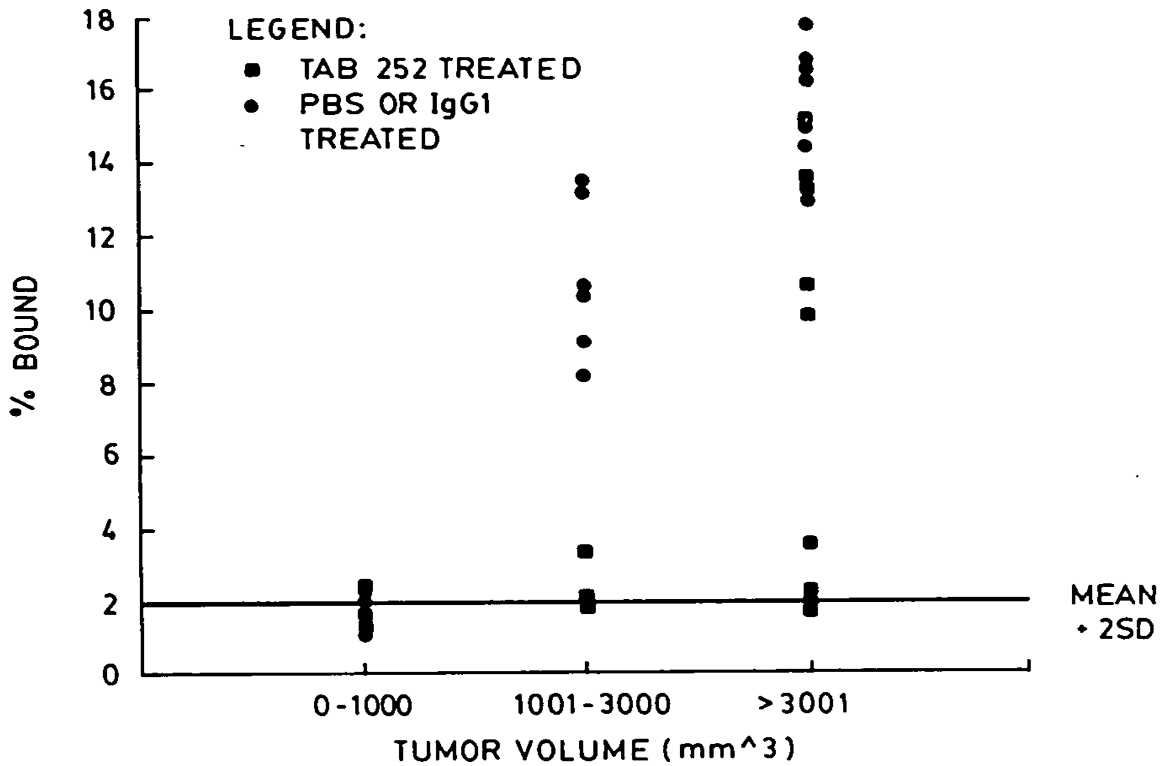


FIG. 10

Analysis of Normal Human Sera in the c–erbB–2 IRMA

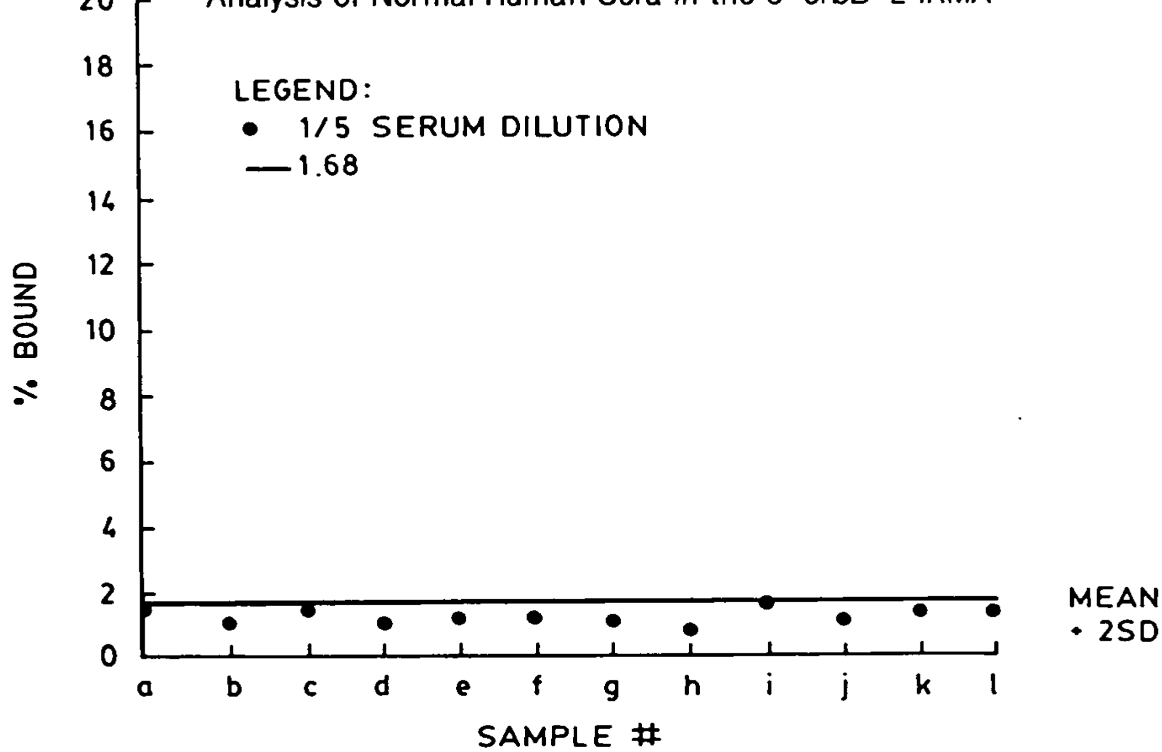


FIG. 11

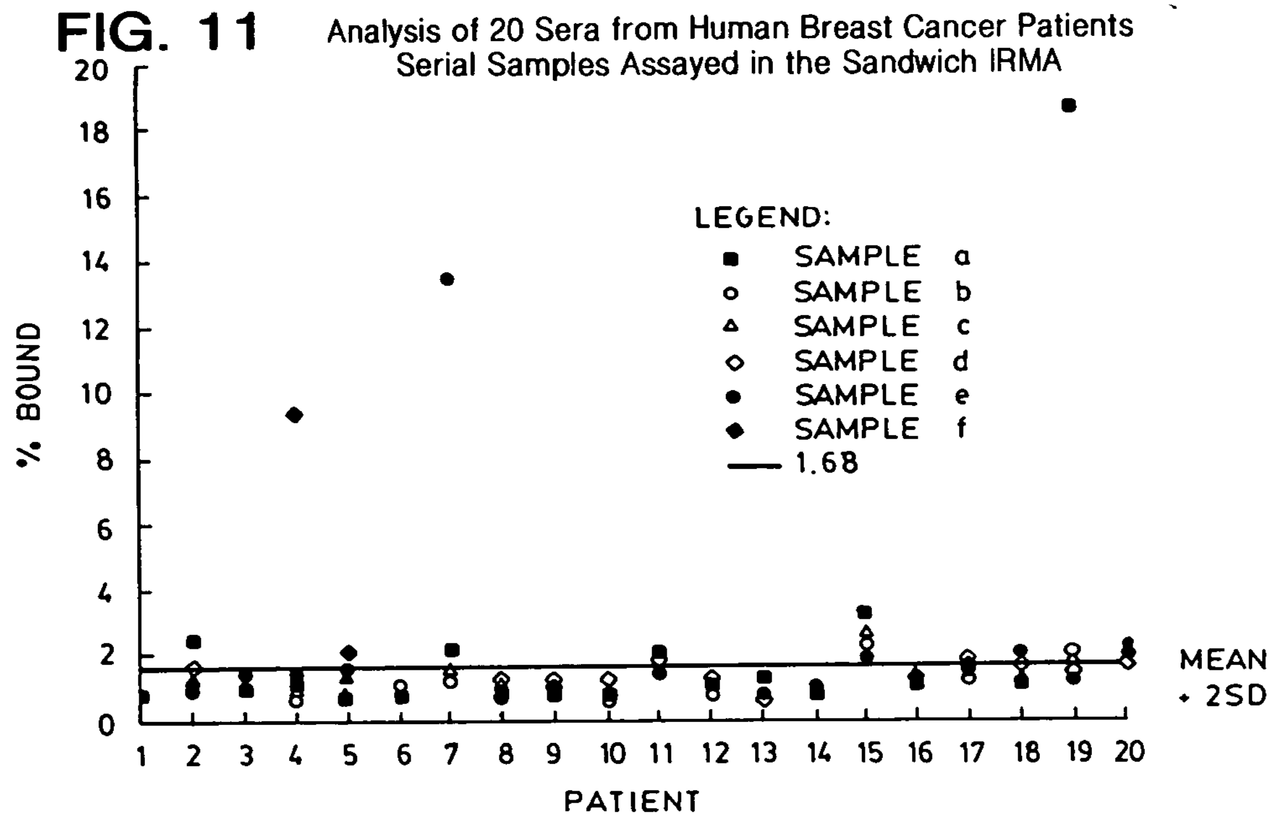

Analysis of 20 Sera from Human Breast Cancer Patients
Serial Samples Assayed in the Sandwich IRMA
% BOUND
LEGEND:
SAMPLE a
SAMPLE b
SAMPLE c
SAMPLE d
SAMPLE e
SAMPLE f
1.68
MEAN
+ 2SD
PATIENT

FIG. 12

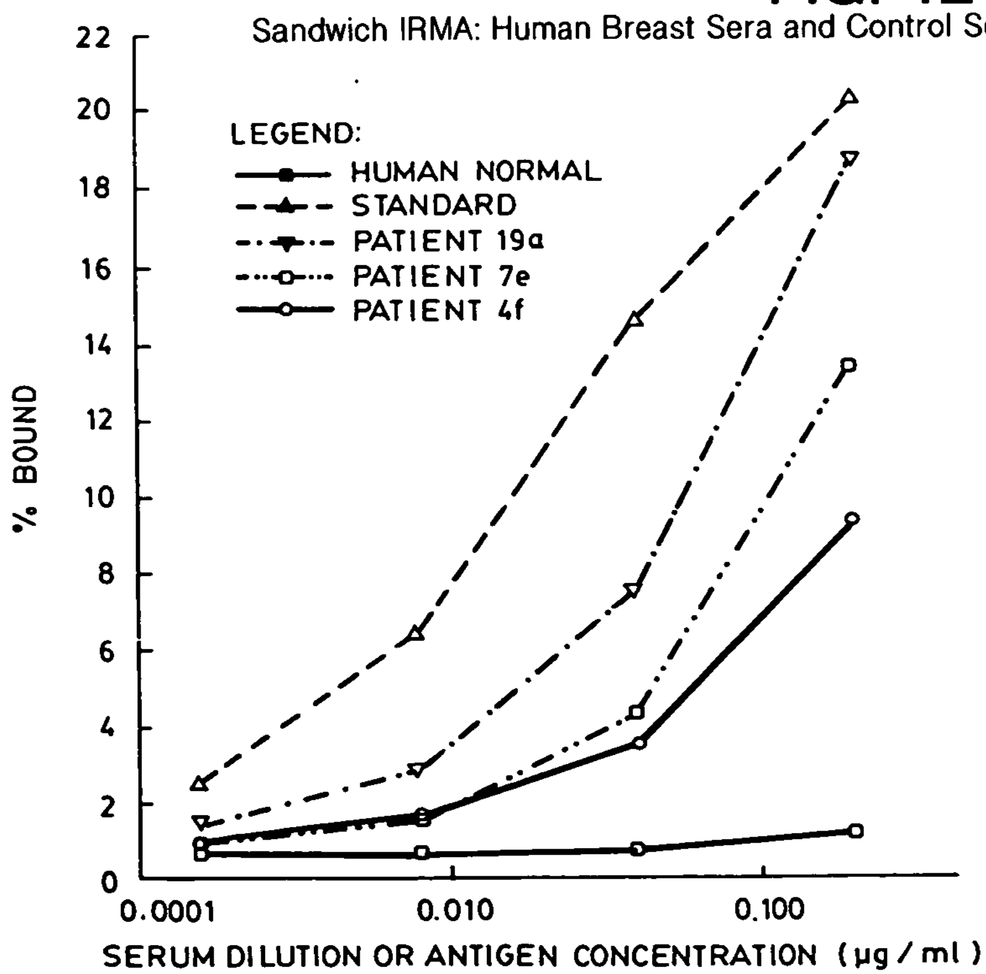
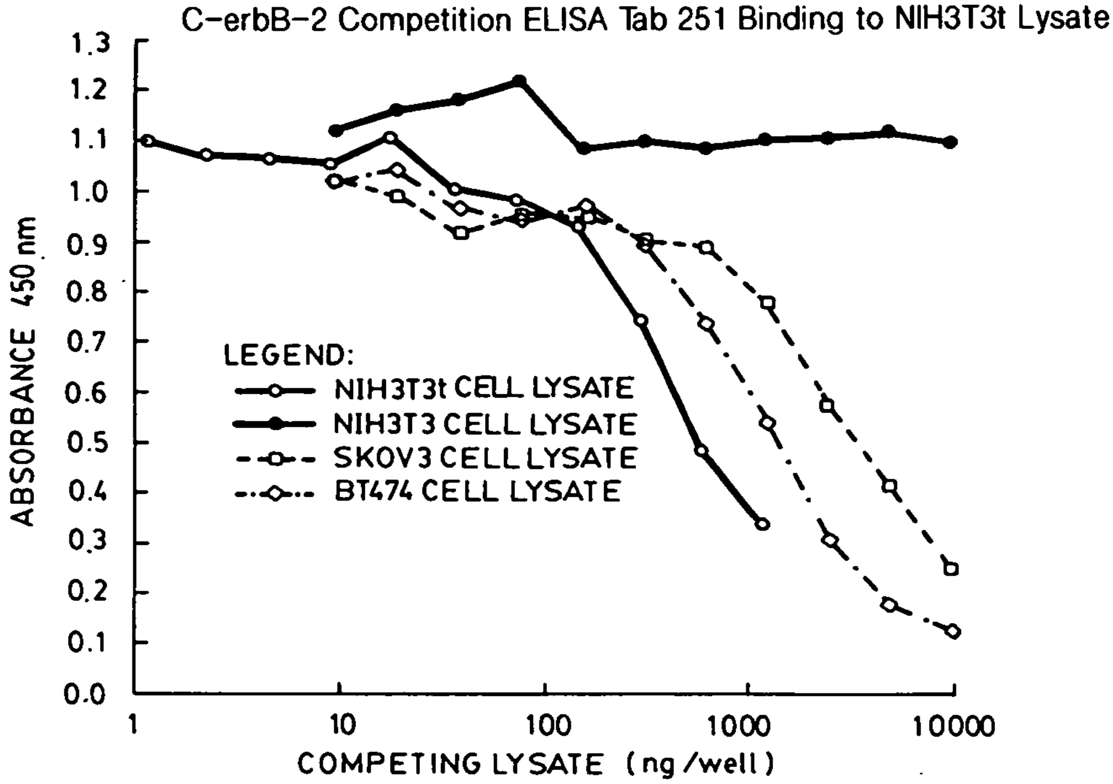
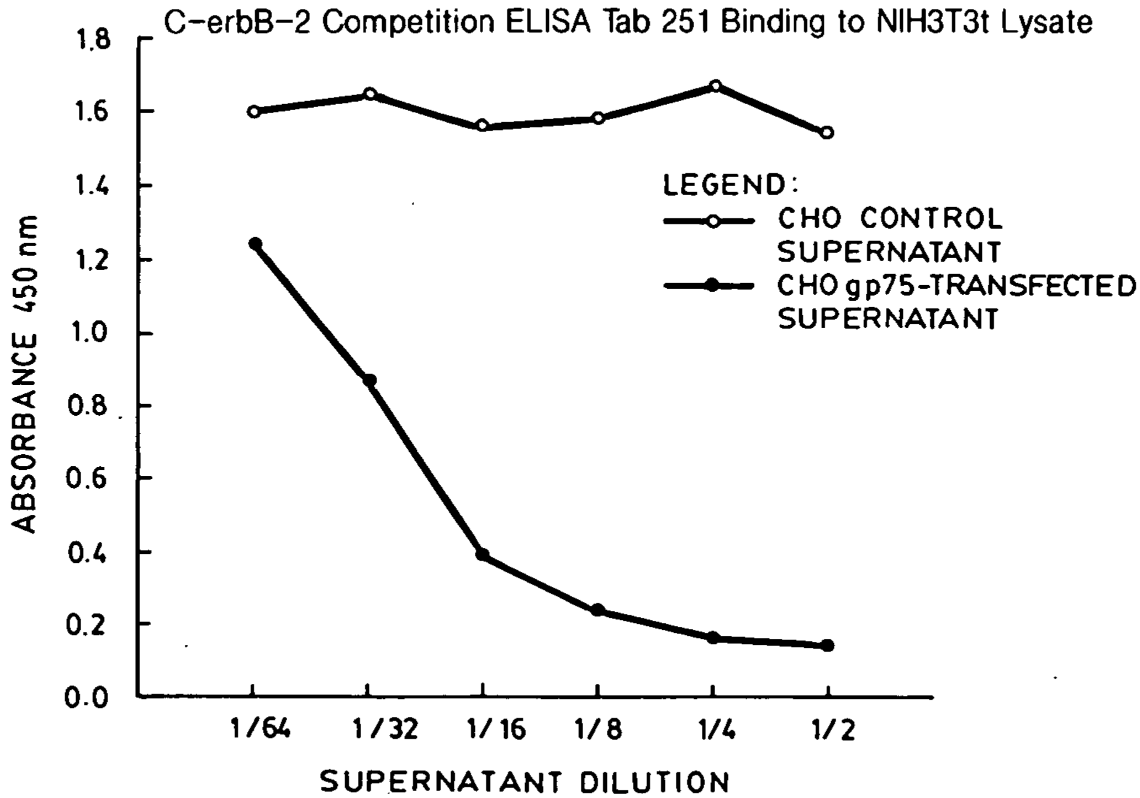

Sandwich IRMA: Human Breast Sera and Control Sera
% BOUND
LEGEND:
HUMAN NORMAL
STANDARD
PATIENT 19a
PATIENT 7e
PATIENT 4f
SERUM DILUTION OR ANTIGEN CONCENTRATION (μg / ml)

FIG. 13



C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate
ABSORBANCE 450 nm
1.3
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1
10
100
1000
10000
COMPETING LYSATE (ng/well)
LEGEND:
NIH3T3t CELL LYSATE
NIH3T3 CELL LYSATE
SKOV3 CELL LYSATE
BT474 CELL LYSATE

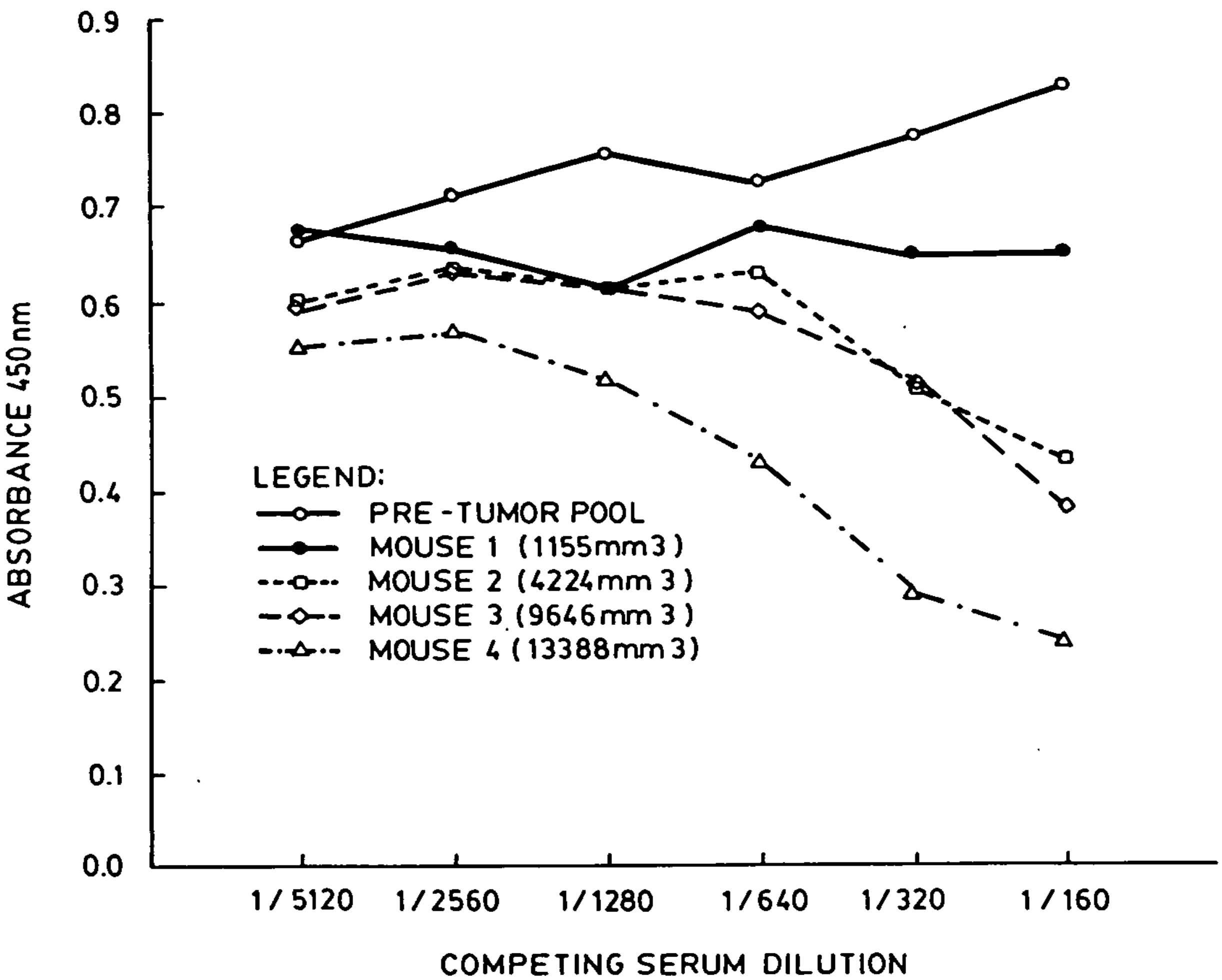
FIG. 14



C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate
ABSORBANCE 450 nm
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1/64
1/32
1/16
1/8
1/4
1/2
SUPERNATANT DILUTION
LEGEND:
CHO CONTROL SUPERNATANT
CHO gp75-TRANSFECTED SUPERNATANT

FIG. 15

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate



1 AATTCTCGAGCTCGTCGACCGGTCGACGAGCTCGAGGGTCGACGAGC

1 10

MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLe

151 ATGGAGCTGGCGGCCTTSTGCCGCTGGGGGCTCCTCCTCGCCCTCTT

60

GlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThrTyrLeuPr

301 CAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAACTCACCTACCTGCC

110

IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaVa

451 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGT

160

GlyGlyValLeuIleGlnArgAsnProGlnLeuCysTyrGlnAspTh

601 GGAGGGGTCTTGATCCAGCGGAACCCCCAGCTCTGCTACCAGGACAC

210

GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuTh

751 GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTCAGAGCCTGAC

260

AspCysLeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLe

901 GACTGCCTGGCCTGCCTCCACTTCAACCACAGTGGCATCTGTGAGCT

310

TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysPr

1051 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCC

360

ArgGluValARgAlaValThrSerAlaAsnIleGlnGluPheAlaGl

1201 CGAGAGGTGAGGGCAGTTACCAGTGCCAATATCCAGGAGTTTGCTGG

410

GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpPr

1351 GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCC

460

SerTrpLeuGlyLeuArgSerLeuArgGluLeuGlySerGlyLeuAl

1501 AGCTGGCTGGGGCTGCGCTCACTGAGGGAACTGGGCAGTGGACTGGC

510

GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAl

1651 GAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGC

560

ProArgGluTyrValAsnAlaArgHisCysLeuProCysHisProGl

1801 CCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCGTGCCACCCTGA

610

ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPh

1951 CCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTT

FIG. 16A

TCGAGGGCGCGCGCCCGGCCCCCACCCCTCGCAGCACCCCGCGCCCCCGC

20 30
uProProGlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLe
GCCCCCCGGAGCCGCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCT

70 80
oThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTy
CACCAATGCCAGCCTGTCCTTCCTGCAGGATATCCAGGAGGTGCAGGGCTA

120 130
lLeuAspAsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSe
GCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTC

170 180
rIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeuThrLe
GATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCTCTCACACT

220 230
rArgThrValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProTh
GCGCACTGTCTGTGCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCAC

270 280
uHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMetPr
GCACTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAGTCCATGCC

320 330
oLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgCysGluLy
CCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAA

370 380
yCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPheAspGl
CTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGCTTTGATGG

420 430
oAspSerLeuProAspLeuSerValPheGlnAsnLeuGlnValIleArgGl
GGACAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGG

470 480
aLeuIleHisHisAsnThrHisLeuCysPheValHisThrValProTrpAs
CCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTGCCCTGGGA

520 530
aArgArgAlaLeuLeuGlySerGlyProThrGlnCysValAsnCysSerGl
CCGCAGGGCACTGCTGGGGTCAGGGCCCACCCAGTGTGTCAACTGCAGCCA

570 580
uCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAlaAspGl
GTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGACCA

620 630
eProAspGluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSe
TCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTC

FIG. 16B

```
CCTCCCAGCCGGGTCCAGCCGGAGCCATGGGGCCGGAGCCGCAGTGAGCACC
                          40                          50
uArgLeuProAlaSerProGluThrHisLeuAspMetLeuArgHisLeuTyr
GCGGCTCCCTGCCAGTCCCGAGACCCACCTGGACATGCTCCGCCACCTCTAC
                          90                         100
rValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
CGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGG
                         140                         150
rProGlyGlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLys
CCCAGGAGGCCTGCGGGAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAA
                         190                         200
uIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
GATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG
                         240                         250
rAspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSer
TGACTGCTGCCATGAGCAGTGTGCTGCCGGCTGCACGGGCCCCAAGCACTCT
                         290                         300
oAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
CAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCC
                         340                         350
sCysSerLysProCysAlaArgValCysTyrGlyLeuGlyMetGluHisLeu
GTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTG
                         390                         400
yAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
GGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT
                         440                         450
yArgIleLeuHisAsnGlyAlaTyrSerLeuThrLeuGlnGlyLeuGlyIle
ACGAATTCTGCACAATGGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATC
                         490                         500
pGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
CCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA
                         540                         550
nPheLeuArgGlyGlnGluCysValGluGluCysArgValLeuGlnGlyLeu
GTTCCTTCGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTC
                         590                         600
nCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys
GTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGC
                         640                         650
rCysValAspLeuAspAspLysGlyCysProAlaGluGlnArgAlaSerPro
CTGTGTGGACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCT
```

FIG. 16C

660
LeuThrSerIleValSerAlaValValGlyIleLeuLeuValValVa
2101 CTGACGTCCATCGTCTCTGCGGTGGTTGGCATTCTGCTGGTCGTGGT

710
ThrProSerGlyAlaMetProAsnGlnAlaGlnMetArgIleLeuLy
2251 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAA

760
AlaIleLysValLeuArgGluAsnThrSerProLysAlaAsnLysGl
2401 GCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAAGCCAACAAAGA

810
MetProTyrGlyCysLeuLeuAspHisValArgGluAsnArgGlyAr
2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACG

860
ValLeuValLysSerProAsnHisValLysIleThrAspPheGlyLe
2701 GTGCTGGTCAAGAGTCCCAACCATGTCAAAATTACAGACTTCGGGCT

910
HisGlnSerAspValTrpSerTyrGlyValThrValTrpGluLeuMe
2851 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGAT

ValTyrMetIleMetValLysCysTrpMetIleAspSerGluCysAr
3001 GTCTACATGATCATGGTCAAATGTTGGATGATTGACTCTGAATGTCG

1010
AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAs
3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGA

1060
SerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSe
3301 TCTACCAGGAGTGGCGGTGGGGACCTGACACTAGGGCTGGAGCCCTC

1110
LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspPr
3451 CTCCCCACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCC

1160
SerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaTh
3601 TCGCCCCGAGAGGGCCCTCTGCCTGCTGCCCGACCTGCTGGTGCCAC

1210
GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAl
3751 GGAGGAGCTGCCCCTCAGCCCCACCCTCCTCCTGCCTTCAGCCCAGC

1255
LeuAspValProValEND
3901 CTGGACGTGCCAGTGTGAACCAGAAGGCCAAGTCCGCAGAAGCCCTG
4051 CTAAGGAACCTTCCTTCCTGCTTGAGTTCCCAGATGGCTGGAAGGGG
4201 CCCTTTCCTTCCAGATCCTGGGTACTGAAAGCCTTAGGGAAGCTGGC
4351 ATGGTGTCAGTATCCAGGCTTTGTACAGAGTGCTTTTCTGTTTAGTT
4501 TTGTCCATTTGCAAATATATTTTGGAAAACAAAAAAAAAAAAAA

FIG. 16D

670 680
lLeuGlyValValPheGlyIleLeuIleLysArgArgGlnGlnLysIleAr
CTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATCCG

720 730
sGluThrGluLeuArgLysValLysValLeuGlySerGlyAlaPheGlyTh
AGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCAC

770 780
uIleLeuAspGluAlaTyrValMetAlaGlyValGlySerProTyrValSe
AATCTTAGACGAAGCATACGTGATGGCTGGTGTGGCTCCCATATGTCTC

830
gLeuGlySerGlnAspLeuLeuAsnTrpCysMetGlnIleAlaLysGlyMe
CCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGAT

870 880
uAlaArgLeuLeuAspIleAspGluThrGluTyrHisAlaAspGlyGlyLy
GGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGGCAA

920 930
tThrPheGlyAlaLysProTyrAspGlyIleProAlaArgGluIleProAs
GACTTTTGGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGA

970 980
gProArgPheArgGluLeuValSerGluPheSerArgMetAlaArgAspPr
GCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGACCC

1020 1030
pLeuValAspAlaGluGluTyrLeuValProGlnGlnGlyPhePheCysPr
CCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCC

1070 1080
rGluGluGluAlaProArgSerProLeuAlaProSerGluGlyAlaGlySe
TGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGGCTGGCTC

1120 1130
oThrValProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCy
CACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTTGCCCCCCTGACCTG

1170 1180
rLeuGluArgAlaLysThrLeuSerProGlyLysAsnGlyValValLysAs
TCTGGAAAGGGCCAAGACTCTCTCCCCAGGGAAGAATGGGGTCGTCAAAGA

1220 1230
aPheAspAsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaPr
CTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGAGCGGGGGGCTCC

ATGTGTCCTCAGGGAGCAGGGAAGGCCTGACTTCTGCTGGCATCAAGAGGT
TCCAGCCTCGTTGGAAGAGGAACAGCACTGGGGAGTCTTTGTGGATTCTGA
CTGAGAGGGGAAGCGGCCCTAAGGGAGTGTCTAAGAACAAAAGCGACCCAT
TTTACTTTTTTTGTTTTGTTTTTTTAAAGACGAAATAAAGACCCAGGGGAG

FIG. 16E